AMENDMENT TO THE CLAIMS

Kindly amend claims 1 and 7 as follows.

1. (Amended) A method of identifying a mammal having or at risk of acquiring a proliferative disease, said method comprising ~~at least one of the~~ following steps:

~~(a) measuring the Sal2 protein level in a cell of said mammal relative to the Sal2 protein level in a mammal not having or being at risk for said proliferative disease;~~

~~(b) determining the presence or absence of an altered Sal2 protein in said mammal relative to a Sal2 protein in a mammal not having or being at risk for a said proliferative disease; or~~

~~(c)~~ determining the presence or absence of a proliferative disease-associated alteration in a *Sal2* nucleic acid in said mammal relative to the nucleic acid sequence of SEQ ID NO.: 2 and SEQ ID NO.:4, ~~wherein a decrease in said SAL2 protein level in step (a) or~~ the presence of an alteration ~~in steps (b) or (c)~~ identifies a mammal as having or being at risk of acquiring a proliferative disease.

2. The method of claim 1, wherein said method is for identifying a mammal having a proliferative disease.

3. The method of claim 1, wherein said method is for identifying a mammal at increased risk of acquiring a proliferative disease.

4. The method of claim 1, wherein said mammal is a human.

5. The method of claim 4, wherein said proliferative disease-associated alteration

comprises the substitution of a Cys for the Ser at position 73 of SEQ ID NO:1.

6. The method of claim 1, wherein said determining is done by polymerase chain reaction (PCR) amplification, single nucleotide polymorphism (SNP) determination, restriction fragment length polymorphism (RFLP) analysis, hybridization analysis, or mismatch detection analysis.

7. (Amended) The method of claim 1, wherein said method ~~step (c)~~ comprises the steps of:

(i) contacting a first nucleic acid probe which is specific for binding to a human *Sal2* nucleic acid containing a proliferation disease-associated alteration with a nucleic acid from a cell from said mammal under conditions which allow said first nucleic acid probe to anneal to complementary sequences in said cell; and

(ii) detecting duplex formation between said first nucleic acid probe and said complementary sequences.

8. The method of claim 7, wherein said first nucleic acid probe is derived from the human *Sal2* nucleic acid containing a proliferative disease-associated alteration.

9. The method of claim 7, further comprising a second nucleic acid probe, wherein said first and second nucleic acid probes are PCR primers, and wherein said human *Sal2* nucleic acid or a fragment thereof is amplified using PCR between steps (i) and (ii).

10. The method of claim 7, wherein said cell is from a physiological sample containing abnormally proliferating tissue.

11. The method of claim 7, wherein said cell is from a physiological sample of

normal tissue.

12. The method of claim 7, wherein said alteration comprises the substitution of a Cys for the Ser at position 73 of SEQ ID NO:1.